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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/047,991

DATE: 05/28/2002  
 TIME: 09:24:23

Input Set : A:\Hmv08001.app  
 Output Set: N:\CRF3\05282002\J047991.raw

**ENTERED**

3 <110> APPLICANT: REED, ROBIN  
 4 ZHOU, ZHAOLAN  
 6 <120> TITLE OF INVENTION: PURIFICATION OF FUNCTIONAL RIBONUCLEOPROTEIN COMPLEXES  
 8 <130> FILE REFERENCE: Hmv-080.01  
 10 <140> CURRENT APPLICATION NUMBER: 10/047,991  
 11 <141> CURRENT FILING DATE: 2002-01-14  
 13 <150> PRIOR APPLICATION NUMBER: 60/261,521  
 14 <151> PRIOR FILING DATE: 2001-01-12  
 16 <160> NUMBER OF SEQ ID NOS: 12  
 18 <170> SOFTWARE: PatentIn Ver. 2.1  
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 21 <211> LENGTH: 393  
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 23 <213> ORGANISM: Enterobacteria phage MS2  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS  
 27 <222> LOCATION: (1)..(390)  
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 31 Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Thr  
 32 1 5 10 15  
 34 ggc gac gtg act gtc gcc cca agc aac ttc gct aac ggg gtc gct gaa 96  
 35 Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu  
 36 20 25 30  
 38 tgg atc agc tct aac tcg cgt tca cag gct tac aaa gta acc tgt agc 144  
 39 Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser  
 40 35 40 45  
 42 gtt cgt cag agc tct gcg cag aat cgc aaa tac acc atc aaa gtc gag 192  
 43 Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu  
 44 50 55 60  
 46 gtg cct aaa gtg gca acc cag act gtt ggt ggt gta gag ctt cct gta 240  
 47 Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val  
 48 65 70 75 80  
 50 gcc gca tgg cgt tcg tac tta aat atg gaa cta acc att cca att ttc 288  
 51 Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe  
 52 85 90 95  
 54 gct acg aat tcc gac tgc gag ctt att gtt aag gca atg caa ggt ctc 336  
 55 Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu  
 56 100 105 110  
 58 cta aaa gat gga aac ccg att ccc tca gca atc gca gca aac tcc ggc 384  
 59 Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly  
 60 115 120 125  
 62 atc tac taa 393

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63 Ile Tyr
64      130
67 <210> SEQ ID NO: 2
68 <211> LENGTH: 130
69 <212> TYPE: PRT
70 <213> ORGANISM: Enterobacteria phage MS2
72 <400> SEQUENCE: 2
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74      1          5          10          15
76 Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
77      20          25          30
79 Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
80      35          40          45
82 Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
83      50          55          60
85 Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
86      65          70          75          80
88 Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
89      85          90          95
91 Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
92      100          105          110
94 Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
95      115          120          125
97 Ile Tyr
98      130
101 <210> SEQ ID NO: 3
102 <211> LENGTH: 1380
103 <212> TYPE: DNA
104 <213> ORGANISM: Escherichia coli
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108 tacttggtga tacgagtctg cgcgtctttc agggcttcat cgacagtctg acgaccgctg 120
109 gcggcggtga tcaccgcagt acgcacggca taccagaaag cggacatctg cgggatgttc 180
110 ggcatgattt cacttttctg ggcgttttcc atggtggcgc caatacgtgg atctttcgcc 240
111 aactcttcct cgtaagactt cagcgctacg gcaccagcg gtttgtcttt attaaccgct 300
112 tccagacctt catcagtcag cagatagttt tcgaggaact ctttcgccag ctctttgttc 360
113 ggactggcgg cgtaataacc tgcgctcagc acgccaacga acggtttgga tggttgacct 420
114 ttgaaggctc gcagtaccgt tacaccataa ttcaacttgc tgggtgcgat gttggacct 480
115 gccacggggc cgttgatggt catcgctggt tcgcctttat taaaggcagc ttctgcgatg 540
116 gagtaatcgg tgtctgcatt catgtgtttg tttttaatca ggtcaaccag gaaggtcaga 600
117 cccgctttcg cgcagcggtt atccacgccc acgtctttaa tgcgtactt gccgttttca 660
118 tacttgaacg cataaccccc gtcagcagca atcagcggcc aggtgaagta cggttcttgc 720
119 aggttgaaca tcagcgcgct cttacctttc gctttcagtt ctttatccag cgccgggata 780
120 tcttccaggg tttttggcgg gttcggcagc agatctttgt tataaatcag cgataacgct 840
121 tcaacagcga tcgggtaagc aatcagcttg ccgttgtaac gtacggcatc ccaggtaaac 900
122 ggatacagct tgtcctggaa cgctttgtcc ggggtgattt cagccaacag gccagattga 960
123 gcgtagccac caaagcggtc gtgtgccagc aagataatgt cagggccatc gccagttgcc 1020
124 gcaacctgtg ggaattttct ttccagttta tccggatgct caacggtgac tttaattccg 1080
125 gtatctttct cgaattttct accgacttca gcgagaccgt tatagccttt atcgccgtta 1140

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126 atccagatta ccagtttacc ttcttcgatt ttggcgagag ccgaggcgga aaacatcatc 1200
127 gtcgttaatg cggataatgc gaggatgcgt gcacctgttt ttattttcat aatctatggt 1260
128 ccttggtggt gaagtgtcgt tgaaaacacc taaacggact ctagtcttctt tatacggcaa 1320
129 cctctttcca tctccttgc ccctacgccc caccgtcgtt ttgtgtgac tctgttacag 1380
132 <210> SEQ ID NO: 4
133 <211> LENGTH: 396
134 <212> TYPE: PRT
135 <213> ORGANISM: Escherichia coli
137 <400> SEQUENCE: 4
138 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
139 1 5 10 15
141 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
142 20 25 30
144 Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
145 35 40 45
147 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
148 50 55 60
150 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
151 65 70 75 80
153 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
154 85 90 95
156 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
157 100 105 110
159 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
160 115 120 125
162 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
163 130 135 140
165 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
166 145 150 155 160
168 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
169 165 170 175
171 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
172 180 185 190
174 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
175 195 200 205
177 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
178 210 215 220
180 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
181 225 230 235 240
183 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
184 245 250 255
186 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
187 260 265 270
189 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
190 275 280 285
192 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
193 290 295 300
195 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
196 305 310 315 320

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198 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
199                               325                               330                               335
201 Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys
202                               340                               345                               350
204 Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala
205                               355                               360                               365
207 Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp
208                               370                               375                               380
210 Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys
211 385                               390                               395
214 <210> SEQ ID NO: 5
215 <211> LENGTH: 44
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
222 <400> SEQUENCE: 5
223 caggatcatat gggatccgcgg gcttctaact ttactcagtt cggt 44
226 <210> SEQ ID NO: 6
227 <211> LENGTH: 44
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
234 <400> SEQUENCE: 6
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238 <210> SEQ ID NO: 7
239 <211> LENGTH: 19
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
245 recognition oligonucleotide
247 <400> SEQUENCE: 7
248 cgtacacat cagggtagc 19
251 <210> SEQ ID NO: 8
252 <211> LENGTH: 17
253 <212> TYPE: PRT
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
258 fusion peptide
260 <400> SEQUENCE: 8
261 Leu Val Pro Arg Gly Ser His Met Arg Gly Ser His His His His His
262 1 5 10 15
264 His
267 <210> SEQ ID NO: 9
268 <211> LENGTH: 7
269 <212> TYPE: PRT

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270 <213> ORGANISM: Artificial Sequence  
 272 <220> FEATURE:  
 273 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 274 thrombin cleavage site peptide  
 276 <400> SEQUENCE: 9  
 277 Leu Val Pro Arg Gly Ser His  
 278 1 5  
 281 <210> SEQ ID NO: 10  
 282 <211> LENGTH: 10  
 283 <212> TYPE: PRT  
 284 <213> ORGANISM: Artificial Sequence  
 286 <220> FEATURE:  
 287 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 288 peptide  
 290 <400> SEQUENCE: 10  
 291 Met Arg Gly Ser His His His His His  
 292 1 5 10  
 295 <210> SEQ ID NO: 11  
 296 <211> LENGTH: 455  
 297 <212> TYPE: DNA  
 298 <213> ORGANISM: Artificial Sequence  
 300 <220> FEATURE:  
 301 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 302 nucleotide sequence  
 304 <400> SEQUENCE: 11  
 305 taatacgact cactataggg agaccggcag atcagcttgg ccgcgtccat ctgggtcatct 60  
 306 aggatctgat atcatcgatg aattcgagct cggtaacccg ttcgtcctca ctctcttccg 120  
 307 catcgctgtc tgcgagggcc agctgttggg gtgagtactc cctctcaaaa gcgggcatga 180  
 308 cttctgccct cgagttatta accctcacta aaggcagtag tcaagggttt ccttgaagct 240  
 309 ttcgtgctga ccctgtccct tttttttcca cagctgcagg tgcacgttga ggacaaactc 300  
 310 ttcgcggtct ttccagtact cttggatccg atatccgtac accatcaggg tacgagctag 360  
 311 cccatggcgt acaccatcag ggtacgacta gtagatctcg tacaccatca gggtacggaa 420  
 312 ttctctagag tcgagttcta tagtgtcacc taaat 455  
 315 <210> SEQ ID NO: 12  
 316 <211> LENGTH: 6  
 317 <212> TYPE: PRT  
 318 <213> ORGANISM: Artificial Sequence  
 320 <220> FEATURE:  
 321 <223> OTHER INFORMATION: Description of Artificial Sequence: 6x His tag  
 323 <400> SEQUENCE: 12  
 324 His His His His His His  
 325 1 5

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/047,991

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